

Display [Full Report](#) Show 20 Sort by Relevance Send to  
 All: 1  Current Only: 1  Genes Genomes  SNP GeneView: 1

1: FGFR3 fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) [Homo sapiens]

GeneID: 2261

updated 08-Jun

[Summary](#)

Official Symbol FGFR3

provided by HG

Official Full Name fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)

provided by HG

Primary source HGNC:3690

See related Ensembl:ENSG00000068078; HPRD:00624; MIM:134934

Gene type protein coding

RefSeq status REVIEWED

Organism *Homo sapiens*

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammali; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Hom

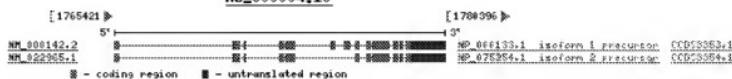
Also known as ACH; CEK2; JTK4; CD333; HSFGFR3EX

**Summary** The protein encoded by this gene is a member of the fibroblast growth factor receptor family, where amino acid sequence is highly conserved between members and throughout evolution. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein would consist of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member binds acidic and basic fibroblast growth hormone and plays a role in bone development and maintenance. Mutations in this gene lead to craniosynostosis and multiple types of skeletal dysplasia. Alternative splicing occurs and additional variants have been described, including those utilizing alternate exon 8 rather than 9, but their full-length nature has not been determined.

### Genomic regions, transcripts, and products

[Go to reference sequence details](#)[Try our new Sequence View](#)

#### NC\_000004.10



---

### Genomic context

---

chromosome: 4; Location: 4p16.3

[See FGFR3 in MapView](#)




---

### Bibliography

---

[Related Articles in PubMed](#)

[PubMed links](#)

[GeneRIFs: Gene References Into Function](#)

1. The technique had a sensitivity and specificity of 100%. CONCLUSION: High resolution melting analysis is a simple, rapid, and sensitive one tube assay genotyping the FGFR3 gene.
2. No sequence variation was found, indicating that mutations in the "hot spot" are not associated with nonsynostotic plagiocephaly.
3. Strong immunohistochemical expression of FGFR3, a superficial staining pattern CK20, and a low proliferative activity define those papillary urothelial neoplasms of low malignant potential that do not recur.
4. Observational study of genotype prevalence and gene-disease association. (HuGE Navigator)
5. Observational study of gene-disease association. (HuGE Navigator)
6. Observational study of genetic testing. (HuGE Navigator)
7. FGFR3 mutation frequency was significantly associated with tumor grade.
8. over-expression of FGFR3 protein in many tumours compared to normal bladder and ureteric controls. Increased expression was associated with mutation (- mutant tumours)
9. MM Patients showing the t(4;14) chromosomal translocation at FGFR3 and genes had a significant elevation of serum crosslaps, reported to be the marker most reliably correlated with the extent of bone resorption
10. analysis of FGFR3 mutation in Muenke syndrome
11. a K650Q mutation in the FGFR3 gene may have a role in Acanthosis nigricans [case report]
12. Mutations were detected in 12 of 13 (92.3%) tumor tissues and 11 of 13 (82% urine samples from patients with superficial bladder cancer).
13. The group of low-grade noninvasive papillary tumours is defined by the presence

an FGFR3 mutation

14. FGFR3 mediates hematopoietic transformation by activating RSK2 in a two-fashion, promoting both the ERK-RSK2 interaction and subsequent phospho of RSK2 by ERK.
15. previously undescribed, heterozygous lysine to threonine mutation at codon the FGFR3 gene in familial acanthosis nigricans
16. Results suggest that a PLCgamma-STAT1 pathway mediates apoptotic sign: FGFR3 in genetic dwarfism and chondrogenic cell lines.
17. the mutant S249C FGFR3 may have a role in bladder cancer
18. Mutations are a possible prognostic tool in survival of urothelial carcinoma of upper urinary tract.
19. FGFR3 may represent a prognostic marker of chromosomally stable bladder with low malignant potential.
20. study showed that FGFR3 mutations appear to be common genetic alterations in multiple seborrheic keratoses with a varying interindividual mutation frequency without specific intraindividual hot spots
21. the fibroblast growth factor family has a pleiotrophic function in human spermatogonia, which physiologically express FGFR3
22. Show preferential occurrence of FGFR3 mutations in seborrheic keratoses on head and neck. Increased age appears to be a risk factor for these mutations
23. analysis of a Chinese family with autosomal dominant achondroplasia; disease locus was mapped to chromosome 4p16.3, where the FGFR3 gene is located. novel Ser217Cys mutation in exon 5 of FGFR3 that causes autosomal dominant achondroplasia was identified
24. Although mutation K650M induces defective targeting of receptor, different mechanism characterized by receptor retention at plasma membrane, excess ubiquitylation and reduced degradation results from mutations of extracellular domain and stop codon.
25. Two patients with clinical and radiological findings of achondroplasia, who have most common FGFR3 missense mutations.
26. G380R mutation of this gene is common mutation associated with achondroplasia
27. involvement of FGFR-3 in malignant hematopoiesis and FGFR-3 tyrosine kinase in CD34+ leukemic cells
28. data indicate that t(4;14)(p16;q32) and loss of fibroblast growth factor receptor occurred at a very early stage of multiple myeloma and suggest that activation of multiple myeloma SET domain protein may be transforming event of this translocation
29. Nucleotide 1138 in transmembrane domain of FGFR3 gene is the hot point mutation in ACH and hence its major pathologic cause.

- 30.FGFR3 expression is significantly associated with two important prognostic stage and grade. Tumours with FGFR3+/p53- phenotype seem to have a distinctive pathway in bladder tumorigenesis.
- 31.identified a heterozygous missense mutation that is predicted to cause a p. substitution in the tyrosine kinase domain and partial loss of FGFR3 function
- 32.no evidence that mosaicism for mutations, normally associated with syndromes of craniosynostosis, occur in single suture craniosynostosis
- 33.results indicate that FGFR 3 plays a crucial role in the accelerated proliferation of MM carrying t(4;14)(p16.3;q32)
- 34.introduction of these mutated FGFR3s into ATDC5 cells downregulated PTHr expression and induced apoptosis with reduction of Bcl-2 expression
- 35.tumors with FGFR3 mutation appear to have distinctive clinical and biologic characteristics that may help in defining a population of patients for FGFR3 mutation screening
- 36.results give further support to the fact that the G380R mutation of FGFR-3 is the most common mutation causing achondroplasia in different populations
- 37.These results suggest that constitutive levels of both FGFR1 and FGFR3, but not FGFR4 are essential for FGF-stimulated anchorage-independent growth of S cells.
- 38.CHEK2 mutation has a role in hereditary breast cancer
- 39.Acanthosis nigricans with achondroplasia due to Gly380Arg mutation in FGFR3
- 40.Reciprocal relationship in gene expression between FGFR1 and FGFR3 in connective tissue plays an important role in the progression of the carcinomas to malignancy
- 41.Mutations were detected in 23 of 27 (85%) adenoid seborrheic keratoses. F mutations were the most frequent mutation type.
- 42.Identification and characterization of an alternatively spliced isoform
- 43.Parathyroid hormone receptor type 1/Indian hedgehog expression is preserved in the growth plate of human fetuses affected with activating mutations in this protein
- 44.there is an FGFR3 mutation with a demonstrated deregulatory mechanism : alternative splicing in the absence of t(4;14) in multiple myeloma patients
- 45.Cherubism was mapped to region 4p16.3. Because of the associated craniosynostosis, we excluded the FGFR3 gene as a candidate gene for cherubism
- 46.defective differentiation of chondrocytes is the main cause of longitudinal bone growth retardation in FGFR3-related human chondrodysplasias
- 47.Differences in spatial patterns of FGFR expression in normal skin may generate functional diversity in response to FGFs, and in wounded skin FGFs may facilitate wound healing via induced FGFRs.

- 48.A missense mutation in FGFR3 resulted in skeletal dysplasia distinct from thanatophoric dysplasia.
- 49.FGFR3 is an important cell survival and antiapoptotic factor for multiple myeloma cells
- 50.the G370C and S371C mutant receptors spontaneously dimerize in the correct spatial orientation required for effective signal transduction, whereas the S371C mutants, like the WT receptor, may achieve this orientation only on ligand binding
- 51.Inhibition of FGFR3 in myeloma cell lines was associated with morphologic, phenotypic, and functional changes typical of plasma cell differentiation, including increase in light-chain secretion and expression of CD31, followed by apoptosis
- 52.FGFR3IIIS may regulate FGF and FGFR trafficking and function, possibly contributing to the development of a malignant phenotype
- 53.Over expression of FGFR3 is associated with urinary tract carcinoma progression
- 54.Gly380 --> Arg mutation does not alter dimerization energetics of FGFR3 transmembrane domain in detergent micelles or lipid bilayers. This indicates that pathogenesis in achondroplasia cannot be explained simply by higher dimer formation of mutant FGFR3.
- 55.phosphorylation is essential for FGFR3 ubiquitylation, but is not sufficient to account for downregulation of its internalization resistant mutants
- 56.mutations in bladder cancer previously identified in non-lethal skeletal disorders
- 57.presence of a Pro250Arg mutation predisposed to an increased transcranial reoperation rate...on the basis of raised intracranial pressure...in apparently "isolated" coronal synostosis
- 58.Review. The role of FGFR3 in endochondral ossification and mutations leading to chondrodysplasia are reviewed.
- 59.First quantitative measurement of mutant receptor tyrosine kinase (RTK) stabilization in the membrane domain environment of FGFR3 shows the predicted effect of resultant increase in the dimer fraction on RTK-mediated signal transduction.
- 60.Results suggest a novel interaction between the SOCS1 and SOCS3 protein and the FGFR3 signaling pathway.
- 61.PRO-001 antibody is a potent and specific inhibitor of FGFR3 and deserves further study for the treatment of FGFR3-expressing myeloma.
- 62.MIP-1 alpha promoter function, gene expression, and protein secretion were down-regulated following inhibition of FGFR3 signaling.
- 63.PIK3CA mutations were strongly associated with FGFR3 mutations in superficial papillary bladder tumors.
- 64.The R248C mutation appears to be a hot spot for FGFR3 mutations in epidermal nevi.

65. FGFR3 gene mutation is found in thanatophoric dysplasia type 1 and bilateral renal dysplasia.
66. Data indicate that after endocytosis, fibroblast growth factor receptor (FGF) its bound ligand, FGF1, are sorted mainly to the recycling compartment, while FGFR1-3 with ligand are sorted mainly to degradation in the lysosomes.
67. For the first time in humans, the expression of basic fibroblast growth factor (bFGF) and its receptors FGFR-2, FGFR-3, and FGFR-4 has been documented in ovaries of second- and third-trimester fetuses.
68. Activating mutations of FGFR3 are associated with benign skin tumors.
69. Mutation in the FGFR3 is associated with progression of oral squamous cell carcinoma.
70. Patients with TWIST gene mutations may have more ophthalmic abnormalities including more strabismus, ptosis, NLDO, astigmatism, vertical deviations, amblyopia compared with patients with FGFR3 gene mutations.
71. The FGFR3-associated coronal synostosis syndrome (Muenke craniostenosis) is caused by a point mutation (C749G) on the FGFR3 gene resulting in a Pro2 substitution.
72. IGF-1 prevents the apoptosis induced by FGFR3 mutation through the PI3K pathway and MAPK pathway.
73. FGFR3 mutation status and loss of 9q is associated with early-stage bladder carcinomas.
74. The present studies show that MUC1 associates with FGFR3.
75. double mutation in FGFR3 encoding GLY380LYS is responsible for Hypochondroplasia.
76. findings indicate that: (1) FGFR3 mutations occur in mosaicism and can cause epidermal nevi and (2) other genes are involved in epidermal nevi.
77. The cell model will be useful for the study of FGFR3 function in cartilage structure and future therapeutic approaches in chondrodysplasias.
78. distribution in normal endocrine cells and related tumors of the gastroenteropancreatic system; immunoreactive in duodenal G cells
79. Mutations in growth factor receptor 3 is associated with the pathogenesis of urothelial cell carcinoma
80. fibroblast growth factor receptor 3 has a role in trafficking and signaling
81. Over-expression of FGFR3 may play an important role in liver carcinogenesis
82. fibroblast growth factor receptor 3 mutations have a role in development of bladder cancer
83. FGFR3 mutations do not seem to play a role in bladder cancer progression
84. We identified a novel ETV6 partner gene, fibroblast growth factor receptor 3 (FGFR3), in a patient with peripheral T-cell lymphoma (PTCL) with a t(4;12)

(p16;p13) translocation.

- 85.FGFR3 and Tp53 mutations do not appear to be associated with progression  
T1G3 transitional bladder carcinomas
- 86.A child who has hypochondroplasia due to an N540K mutation and who has  
temporal lobe dysgenesis.
- 87.the importance of the immature FGFR3 proteins as mediators of an abnorm  
signaling in thanatophoric dysplasia type II
- 88.FGFR3 mutations were associated with low-stage, low-grade urothelial carc  
of the blader.
- 89.strong correlation between mutations of FGFR3 and disturbances of skeletal  
REVIEW
- 90.fibroblast growth factor receptor 3 activation is regulated by cytoplasmic ty  
kinase Pyk2
- 91.The detection of FGFR3 mutations in FUH (Flat Urothelial Hyperplasias) sup  
the role of this lesion as precursor of papillary bladder cancer.
- 92.These results suggest that intracellular domain mutations define a distinct i  
by which mutated FGFR3 could disrupt bone development.
- 93.alternative splicing of FGFR3IIIb results in a secreted isoform that inhibits F  
induced proliferation
- 94.interacts with adapter protein SH2-B, and has a role in STAT5 activation

**Description .....**

Product	Interactant	Other Gene	Complex Source	Pubs
NP_000133.1	NP_067007.3	C6orf47	HPRD	Pu
NP_000133.1	Fibroblast growth factor 1	FGF1	HPRD	Pu
NP_000133.1	Fibroblast growth factor 8	FGF8	HPRD	Pu
NP_000133.1	Fibroblast growth factor 9	FGF9	HPRD	Pu
NP_000133.1	NP_002077.1	GRB2	HPRD	Pu

**General gene information****Markers**

WI-15208(e-PCR)

Links: UniSTS:34762

Alternate names: EST318764; RH59111

G15851(e-PCR)

Links: UniSTS:43116

Alternate names: CHLC.UTR\_02040\_M64347; CHLC.UTR\_02040\_M64347.P56111

RH18137(e-PCR)

Links: UniSTS:91412

GDB:187013(e-PCR)

Links: UniSTS:155533

GDB:454672(e-PCR)

Links: UniSTS:157443

GDB:454675(e-PCR)

Links: UniSTS:157444

GDB:581559(e-PCR)

Links: UniSTS:157858

GDB:585477(e-PCR)

Links: UniSTS:157890

GDB:681581(e-PCR)

Links: UniSTS:158627

## Genotypes

See FGFR3 SNP GeneView Report

See FGFR3 SNP Genotype Report

## Phenotypes

### Achondroplasia

MIM: 100800

### Bladder cancer

MIM: 109800

### CATSHL syndrome

MIM: 610474

### Cervical cancer, somatic

MIM: 603956

### Colorectal cancer, somatic

MIM: 109800

### Crouzon syndrome with acanthosis nigricans

MIM: 134934

### Hypochondroplasia

MIM: 146000

### LADD syndrome

MIM: 149730

### Muenke syndrome

MIM: 602849

### Nevus, keratinocytic, nonepidermolytic

MIM: 162900

### Thanatophoric dysplasia, types I and II

MIM: 187600

## Pathways

### KEGG pathway: MAPK signaling pathway

04010

### KEGG pathway: Regulation of actin cytoskeleton

04810

### Reactome Event: Signaling by FGFR

190236

## Homology

### Mouse, Rat

Map Viewer

## GeneOntology

Provided by

Function	Evidence
ATP binding	IEA
fibroblast growth factor receptor activity	NAS
PubMed 7923141	
identical protein binding	

PubMed 14732692	IPI
nucleotide binding	IEA
protein tyrosine kinase activity	IEA
receptor activity	IEA
transferase activity	IEA

Process	Evidence
JAK-STAT cascade	TAS
PubMed 10918587	
MAPKKK cascade	TAS
PubMed 10918587	
cell growth	NAS
fibroblast growth factor receptor signalling pathway	TAS
PubMed 10918587	
protein amino acid phosphorylation	IEA
sensory perception of sound	IEA
skeletal development	TAS
PubMed 8601314	

Component	Evidence
integral to membrane	IEA
integral to plasma membrane	TAS
PubMed 10918587	
plasma membrane	EXP
PubMed 11294897,16597617	

---

#### General protein information

---

Preferred Names  
fibroblast growth factor receptor 3

Names  
fibroblast growth factor receptor 3  
tyrosine kinase JTK4  
hydroxaryl-protein kinase

NP\_000133.1  
EC 2.7.10.1  
NP\_075254.1  
EC 2.7.10.1

---

### NCBI Reference Sequences (RefSeq)

---

#### RefSeqs maintained independently of Annotated Genomes

These reference sequences exist independently of genome builds.

##### mRNA and Protein(s)

###### 1. NM\_000142.3→NP\_000133.1 fibroblast growth factor receptor 3 isoform 1 precursor

Description	Transcript Variant: This variant (1) is missing alternatively spliced exon 8 but utilizes alternatively spliced exon 9, resulting in Isoform (1) with the IIIc-type C-terminal half of the IgIII domain.  AB209441, AC016773, BC153824
Source sequence(s)	AB209441, AC016773, BC153824
Consensus CDS	CCDS3353.1
UniProtKB / Swiss-Prot	P22607
Conserved Domains (5) summary	<p><b>cd00931</b> Location: 151–243 Blast Score: 204</p> <p><b>cd05100</b> Location: 459–753 Blast Score: 1597</p> <p><b>plam07714</b> Location: 472–748 Blast Score: 987</p> <p><b>cI00093</b> Location: 253–346 Blast Score: 132 Location: 55–110 Blast Score: 103</p> <p><b>IGCam</b>; Immunoglobulin domain cell adhesion molecule (cam) subfamily; members are components of neural cell adhesion molecules (N-CAM L1), Fasciclin II and the insect immune protein Hemolin. The subfamily also includes receptor domains such as the...</p> <p><b>PTKc_FGFR3</b>; PTKc_FGFR3: Protein Tyrosine Kinase (PTK) family; Fibroblast Growth Factor Receptor 3 (FGFR3); catalytic (c) domain. The PTKc family is part of a larger superfamily that includes the catalytic domains of other kinases such as protein serine/threonine...</p> <p><b>PKinase_Tyr</b>; Protein tyrosine kinase.</p> <p><b>IG</b>; Immunoglobulin domain family; members are components of immunoglobulins, neuroglia, cell surface glycoproteins, such as, T-cell receptors, CD2, CD4, CD8, and membrane glycoproteins, such as, butyrophilin and chondroitin sulfate proteoglycan core...</p>

###### 2. NM\_022965.2→NP\_075254.1 fibroblast growth factor receptor 3 isoform 2 precursor

Description	Transcript Variant: This variant (2) does not contain alternatively spliced exons 8 or 9, resulting in a loss of the C-terminal half of the IgIII domain. In addition, this variant is missing alternatively spliced exon 10 which encodes the transmembrane region, suggesting a soluble receptor.  AB209441, AC016773, AF245114
Source sequence(s)	AB209441, AC016773, AF245114
Consensus CDS	CCDS3354.1
Conserved Domains (4) summary	<p><b>cd00931</b> Location: 151–243 Blast Score: 203</p> <p><b>plam07714</b> Location: 380–636 Blast Score: 984</p> <p><b>cI00093</b> Location: 53–110</p> <p><b>IGCam</b>; Immunoglobulin domain cell adhesion molecule (cam) subfamily; members are components of neural cell adhesion molecules (N-CAM L1), Fasciclin II and the insect immune protein Hemolin. The subfamily also includes receptor domains such as the...</p> <p><b>PKinase_Tyr</b>; Protein tyrosine kinase.</p> <p><b>IG</b>; Immunoglobulin domain family; members are components of immunoglobulins, neuroglia, cell</p>

---

RefSeqs of Annotated Genomes: Build 36.3

---

The following sections contain reference sequences that belong to a specific genome build.

Reference assembly

---

*Genomic*

1. NC\_00004.10 Reference assembly
 

Range	1765421..1780396
Download	<a href="#">GenBank</a> <a href="#">FASTA Sequence Viewer (beta)</a>
  
2. NT\_006081.18
 

Range	301275..316250
Download	<a href="#">GenBank</a> <a href="#">FASTA Sequence Viewer (beta)</a>

---

Alternate assembly (based on Celera assembly)

---

*Genomic*

1. AC\_000047.1 Alternate assembly (based on Celera assembly)
 

Range	1708138..1723112
Download	<a href="#">GenBank</a> <a href="#">FASTA Sequence Viewer (beta)</a>
  
2. NW\_921918.1
 

Range	1708138..1723112
Download	<a href="#">GenBank</a> <a href="#">FASTA Sequence Viewer (beta)</a>

---

Alternate assembly (based on HuRef)

---

*Genomic*

1. AC\_000136.1 Alternate assembly (based on HuRef)
 

Range	1753471..1738498, complement
Download	<a href="#">GenBank</a> <a href="#">FASTA Sequence Viewer (beta)</a>
  
2. NW\_001838896.2
 

Range	2015637..2000664, complement
Download	<a href="#">GenBank</a> <a href="#">FASTA Sequence Viewer (beta)</a>

---

Related Sequences

---

Nucleotide

Protein

Genomic	AC016773.8 (170070..185045)	None
Genomic	AF487554.1	AAM22078.1
		AAM22079.1
Genomic	AY768549.1	AAU89726.1
Genomic	CH471131.2	EAW82562.1
		EAW82563.1
		EAW82564.1
		EAW82565.1
		EAW82566.1
		EAW82567.1
		EAW82568.1
Genomic	S76733.1	AAB33323.1
Genomic	U22410.1	AAA67781.1
mRNA	AB209441.1	BAD92678.1
mRNA	AF238374.1	AAF97749.1
mRNA	AF245114.1	AAF63380.1
mRNA	AF369211.1	AAK54727.1
mRNA	AF369212.1	AAK54728.1
mRNA	AF369213.1	AAK54729.1
mRNA	BC121175.2	AAI21176.1
mRNA	BC128610.1	AAI28611.1
mRNA	BC153824.1	AAI53825.1
mRNA	M58051.1	AAA52450.1
mRNA	M59374.1	AAA63209.1
mRNA	M64347.1	AAA58470.1
mRNA	X84939.1	CAA59334.1
Synthetic	BC166684.1	AAI66684.1

Protein Accession	Links
P22607.1	GenPept UniProtKB/Swiss-Prot
Q01J44	GenPept UniProtKB/TrEMBL
Q59FL9	GenPept UniProtKB/TrEMBL
Q8NI15	GenPept UniProtKB/TrEMBL
Q8NI16	GenPept UniProtKB/TrEMBL
Q96T34	GenPept UniProtKB/TrEMBL
Q96T35	GenPept UniProtKB/TrEMBL
Q96T36	GenPept UniProtKB/TrEMBL
Q9NRB6	GenPept UniProtKB/TrEMBL

---

### Additional Links

---

- MIM 134934
- GeneTests for MIM: 100800
- GeneTests for MIM: 134934
- HPRD 00624
- UniGene Hs.1420

Display  Show

[Write to the Help Desk](#)  
NCBI NLM NIH  
Department of Health & Human Services  
[Privacy Statement](#) | [Freedom of Information Act](#) | [Disclaimer](#)